

SVIS D1  
cont

(b) a processing means, wherein said processing means transforms said data into a model representing at least a portion of the Ce3 or Ce4 domain from the Fc-region of an IgE protein.

22. (New) The data processing system of Claim 21, wherein said IgE protein is a human IgE protein.

23. (New) The data processing system of Claim 21, wherein said data represents the atomic coordinates of protein backbone atoms having a root mean square deviation less than 10 angstroms from the human IgE protein Ce3 or Ce4 domain backbone atoms defined by the atomic coordinates represented in Table 1, Table 2 or Table 3.

AI  
cont

24. (New) The data processing system of Claim 21, wherein said data represents the atomic coordinates of backbone atoms from a protein having an amino acid sequence at least 80% homologous to the amino acid sequence of SEQ ID NO:2.

25. (New) The data processing system of Claim 21, wherein said data represents at least a portion of the atomic coordinates listed in Table 1, Table 2 or Table 3.

26. (New) The data processing system of Claim 21, wherein said data consists of the atomic coordinates listed in Table 1, Table 2 or Table 3.

27. (New) The data processing system of Claim 21 further comprising a display means for displaying said model.

28. (New) A method to produce a three-dimensional model of the Ce3 or Ce4 domain of the Fc-region of a non-human IgE protein, said method comprising:

(a) obtaining a three-dimensional model of the Ce3 or Ce4 domain from the Fc-region of the human IgE protein using the data processing system of Claim 22;

(b) obtaining the amino acid sequence of a non-human IgE protein;

(c) comparing the Ce3 or Ce4 domain amino acid sequence from the non-human IgE protein with the Ce3 or Ce4 domain amino acid sequence from the human IgE protein;

(d) at positions at which the two sequences differ, replacing the amino acids in the three-dimensional model of the human IgE with the amino acid from the corresponding position of the non-human IgE protein sequence to create a three-dimensional model of the non-human IgE protein; and

(e) displaying said three-dimensional model of the non-human protein on a display means.

29. (New) The method of Claim 28, wherein said three-dimensional model of the human IgE protein is obtained using the atomic coordinates listed in Table 1, Table 2 or Table 3.

30. (New) A method to produce a three-dimensional model of the Ce3 or the Ce4 domain of the Fc-region of the human IgE protein, said method comprising:

(a) obtaining a first set of data representing the atomic x-ray crystallographic coordinates that define the relative position of amino acids from at least a portion of the Ce3 or Ce4 domain from the Fc-region of the human IgE protein;

(b) transforming said first set of data into a second set of data representing a three-dimensional model; and

(c) displaying said data representing said three-dimensional model.

31. (New) The method of Claim 30, wherein the crystallographic coordinates of (a) are selected from Table 1, Table 2 or Table 3.

32. (New) The method of Claim 30, wherein said first set of data is obtained by the steps of:

(i) obtaining a protein crystal comprising at least the Ce3 or at least the Ce4 domain from the Fc region of the human IgE protein;

(ii) producing diffraction data from said protein crystal; and

(iii) transforming said diffraction data into data representing atomic coordinates of said protein comprising at least the Ce3 or at least the Ce4 domain from the Fc region of the human IgE protein.

33. (New) The method of Claim 32, wherein the protein crystal is produced using the hanging drop or the vapor diffusion method, wherein the protein comprising the Ce3 or Ce4

domain from the Fc-region of the human IgE protein is concentrated in a solution comprising about 10 mM Tris-(hydroxymethyl)aminomethane at about pH 8.0, and crystallization is performed using a precipitant composed of about 25 mM sodium acetate at a pH of about 4.6 and 33% polyethylene glycol 4000.

34. (New) The method of Claim 32, wherein the protein crystal belongs to the space group P4<sub>2</sub>1<sub>2</sub> with unit cell dimensions of a equals about 105 Å, b equals about 105 Å and c equals about 47 Å.

35. (New) The method of Claim 30, wherein said three-dimensional model is displayed as a set of atomic coordinates, a physical three-dimensional model, an image on a computer screen, a picture of said model or a set of coordinates derived from a picture of said model.

AI  
Cond  
36. (New) A method to identify a compound that inhibits the binding between an IgE antibody and a FcεRIα protein, said method comprising:

(a) using a three-dimensional model of the Ce3 or Ce4 domain of the Fc-region from a human IgE protein to identify a compound capable of inhibiting the binding between an IgE antibody and a FcεRIα protein; and

(b) testing said compound in an IgE/ FcεRIα protein binding assay to determine if it inhibits binding of IgE to a FcεRIα protein.

37. (New) The method of Claim 36, wherein the three-dimensional model of (a) is represented by the atomic coordinates listed in Table 1, Table 2 or Table 3.

38. (New) The method of Claim 36, wherein step (a) comprises:

- (i) obtaining a 3-dimensional model of the Ce3 or Ce4 domains from the Fc-region of the human IgE protein;
- (ii) obtaining a 3-dimensional model of a compound; and
- (iii) assessing whether said compound model and said model of the Ce3 or Ce4 domains from the Fc-region of the human IgE protein associate through stable interactions, wherein such interactions indicate the compound is capable of inhibiting the binding of an IgE antibody to a FcεRIα protein;